

[illegible]

JOURNAL	Submitted (23-MAR-2001) New Laboratory of Crop Cytogenetics.
FEATURES	Nanjing Agricultural University, Nanjing, Jiangsu, China
Source	Location/Qualifiers
CDS	/organism="Triticum aestivum"
	/db_xref="taxon:4565"
	/codon_start=1
	/product="Mg1 protein"
	/protein_id="AF158971"
	/translation="Mg1 protein"
	/rerna_name="Mg1 protein"
	WIKIRIKI NALON, B. KALAYDAR, I. SEL, LAYDAR, I. SOGLI, I. PEKAR, I. KIRK, I. KIR

AAFP24585
ID AAFP24585 standard; DNA; 1886 BP

AC AAF24585;

DT 20-APR-2001 (first entry)

DE Nucleotide sequence of the wheat M10 protein Tm103

KW wheat; fungal resistance; fungal pathogen; *Erysiphe graminis*; papillae.

XX

05 Trilecium sp.

FH	Key	Location/Qualifiers
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PT /#Lbg= A

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PA (NOVS) NOVARTIS-ERFINDUNGS-

PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM, Wang HX

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DR P-PSDB; AAB31252.

PT Novel polynucleotid

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CC resistance to fungal pathogens which

CC Erysiphe graminis (powdery mildews). In barley, mutations at the Mlo

CC of M10 resistance involves the formation of large cell wall appositions,

CC callose, but also carbohydrates, phenols and proteins. Polynucleotides

CC preferably wheat, which are resistant to fungal pathogens.

Sequence 1886 BP; 405 A; 564 C; 531 G; 386 T; 0 other;

Query Match 91.88; Score 1570.6; DB 22; Length 1886;

Matches 1615; Conservative 0; Mismatches 74; Indels 0; Gaps

QY 1 ATGGCGAGGACTACGAGTACCCCGGCGGCGACGCTGCCGAGACGCCCTCTGGCG 60

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QY 121 AAGTCGGCAATTGGTTCCACAGAGCGGCACAGAACCGCTGCGCGAGGCGCTGGAGAG 180

Db 318 AGCTGGCGATTGTTCCACAGCGGCACAGAACCGCTGGCGGAGGCCCTGGAGAAG 377

QY 181 ATCAAAGCGAGCTGATGCTGGTGGGTTCAATCTCGCTGCTGCTCCGCCGTACGCCAGGAC 240

Db 378 ATGAGGCGGAGCTGATGCTGCTGGATTCATCTCGCTGCTGCTGCGGCTCACGCAAGAC 437

[illegible]

[illegible][illegible]

Oy 1130 TCATGAAAGTCGTGCTGGGGCTGGCTCTTCAGATTCCTGTGCAAGTAAATTCACCTTCGCC 1189
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Search completed: November 18, 2002, 13:11:39
Job time: 377 secs


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Db 965 TCGTAACTTATTTGTGGACAAAATCTGTAAGTATATATATAAATAGATAGTAA 1024
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Db 1385 AAAATATCA 1394

RESULT 3
US-09-857-896a
Sequence 3048, Application US/0998842A
Patent No. US2002016078A1
GENERAL INFORMATION:
Applicant: Mers, Jean
Applicant: Mers, Jean
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
CURRENT PRIORITY NUMBER: US/99/938,842A
CURRENT FILING DATE: 2001-08-24
PRIORITY NUMBER: US 60/227,866
PRIORITY FILING DATE: 2001-01-16
PRIORITY NUMBER: US 60/264,647
PRIORITY FILING DATE: 2001-06-32
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 2048
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-857-896a-2048
Query Match: 17.1%; Score 327; DB 9; Length 1713;
Mismatch 596; Complement 136; Offset 435; Index 21; Gaps 2;

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Db 524 TAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 583
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RESULT 4
US-09-857-896a-1689
Sequence 1689, Application US/0998842A
Patent No. US2002016078A1
GENERAL INFORMATION:
Applicant: Mers, Jean
Applicant: Mers, Jean
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

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us-09-857-896a-31.rnpb

Page 5

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RESULT 6
US-09-938-842A-2268
Sequence 2266, Application US/09938642A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Krieps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong

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Page 8

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Qy 121 MAACTGGGCAATTTCTCCACAGGGGCGACAGAACCGCTGGCGAGGGCTTGAGAG 180
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Db 7242 GGGGTGCACCTCTCGGGGGGGGAGCGGCGACCGGATCCGATCCCGCGCTGTGTGAAG 7301
Qy 181 ATCAAAGCGGAGCGTAACTGTGGGGGTTCTATCTGCTGCTGCGCGTGAAGCAAG 237
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 7302 CAGCGCGGCACTGCTCTGTGACAGAGCGCACGACGCGCTGTACCGCGGATCTGAG 7358

Search completed: November 18, 2002, 15:35:06
JOS time : 39 sec
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Page 2

[illegible][illegible]

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Page 4

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RESULT 5
US-09-558-679-1
Patent NO. 463728
GENERAL INFORMATION US/09558679
APPLICANT: SIMON, Carl R.
TITLE OF INVENTION: In Plants
FILE REFERENCE: 5718-42A-M03
CURRENT FILING DATE: 2000-04-28
PRIORITY FILING DATE: 1999-07-06
PRIORITY APPLICATION NUMBER: 09/350,268
SOFTWARE: Plantain Var. 2.0
SBO ID NO. 1
SBO ID 1 4659
TYPE: DNA
ORGANISM: zea mays
RELEVANT INFORMATION: M03
US-09-558-679-1

Query Match	14.3%;	Score 244.8;	DB 4;	length 185;
Best Local Similarity	52.9%;	Pred. No. 3.3e-47;		
Matches 707; Conservative	0;	Mismatches 542;	Indels 87;	Gaps 5

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 08 11 GGGGAGAGGCTCCGCGGAGAGAGCGGCTGGGCGGCGGCGGCTGGGCGGCGGAGT 87
 09 94 GAGGAGGAGGCTGGGAGAGAGAGCGGCTGGGCGGCGGCGGCTGGGCGGCGGAGT 151
 10 87 CAGCGCGGCTCCGCGGAGAGAGCGGCTGGGCGGCGGCGGCTGGGCGGCGGAGT 146
 11 07 CAGCGCGGCTCCGCGGAGAGAGCGGCTGGGCGGCGGCGGCTGGGCGGCGGAGT 146
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 15 209 GCGGAGAGAGCGGCGGAGAGAGCGGCTGGGCGGCGGCGGCTGGGCGGCGGAGT 206
 16 07 CCGGAGAGAGCGGCGGAGAGAGCGGCTGGGCGGCGGCGGCTGGGCGGCGGAGT 206
 17 207 GCGGAGAGAGCGGCGGAGAGAGCGGCTGGGCGGCGGCGGCTGGGCGGCGGAGT 206
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 21 269 CCGGAGAGAGCGGCGGAGAGAGCGGCTGGGCGGCGGCGGCTGGGCGGCGGAGT 206

[illegible]

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Query Match	Local Similarity	Score	Length	1831:
Best Local	Similarity	49.0%	Pred	No 4.9e-30
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[illegible]

GENERAL INFORMATION:
 APPLICANT: Gibson, Rebecca E.
 APPLICANT: Miao, Guo-Hua

APPLICANT: Ratselaki, J. Antoni
 APPLICANT: Ratselaki, J. Antoni

TITLE OF INVENTION: CORN DNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
 FILE REFERENCE: BB-1125

CURRENT FILING DATE: 1998-11-02
 EARLIER APPLICATION NUMBER: 60/064,493

NUMBER OF SEQ ID NOS: 0
 SOFTWARE: Microsoft Windows 95

SEQ ID NO 3
 SEQ ID NO 37

TYPE: DNA
 ORGANISM: Zea mays

NAME/KEY: unauze
 LOCATION: (3)

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 LOCATION: (475)

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NAME/KEY: unauze
 LOCATION: (383)

Query Match
 best Local Similarity: 5.28; Score 88.6; DB 4; Length 597;
 Matches: 197; Conservative 0; Mismatch 197; Indels 3; Gaps 1;

GENERAL INFORMATION:
 APPLICANT: Gibson, Rebecca E.
 APPLICANT: Miao, Guo-Hua

APPLICANT: Ratselaki, J. Antoni
 APPLICANT: Ratselaki, J. Antoni

TITLE OF INVENTION: CORN DNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
 FILE REFERENCE: BB-1125

CURRENT FILING DATE: 1998-11-02
 EARLIER APPLICATION NUMBER: 60/064,493

NUMBER OF SEQ ID NOS: 0
 SOFTWARE: Microsoft Windows 95

SEQ ID NO 5
 SEQ ID NO 5

TYPE: DNA
 ORGANISM: Zea mays

NAME/KEY: unauze
 LOCATION: (164)

NAME/KEY: unauze
 LOCATION: (351)

NAME/KEY: unauze
 LOCATION: (351)

NAME/KEY: unauze
 LOCATION: (351)

Query Match
 best Local Similarity: 69.64; P-Ed No. 1.4e-08;
 Matches: 103; Conservative 0; Mismatch 93; Indels 0; Gaps 0;

GENERAL INFORMATION:
 APPLICANT: Gibson, Rebecca E.
 APPLICANT: Miao, Guo-Hua

APPLICANT: Ratselaki, J. Antoni
 APPLICANT: Ratselaki, J. Antoni

TITLE OF INVENTION: CORN DNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
 FILE REFERENCE: BB-1125

CURRENT FILING DATE: 1998-11-02
 EARLIER APPLICATION NUMBER: 60/064,493

NUMBER OF SEQ ID NOS: 0
 SOFTWARE: Microsoft Windows 95

SEQ ID NO 5
 SEQ ID NO 5

TYPE: DNA
 ORGANISM: Zea mays

NAME/KEY: unauze
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NAME/KEY: unauze
 LOCATION: (351)

NAME/KEY: unauze
 LOCATION: (351)

Query Match
 best Local Similarity: 4.44; Score 76; DB 4; Length 750;
 Matches: 103; Conservative 0; Mismatch 93; Indels 0; Gaps 0;

GENERAL INFORMATION:
 APPLICANT: Gibson, Rebecca E.
 APPLICANT: Miao, Guo-Hua

APPLICANT: Ratselaki, J. Antoni
 APPLICANT: Ratselaki, J. Antoni

TITLE OF INVENTION: CORN DNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
 FILE REFERENCE: BB-1125

CURRENT FILING DATE: 1998-11-02
 EARLIER APPLICATION NUMBER: 60/064,493

NUMBER OF SEQ ID NOS: 0
 SOFTWARE: Microsoft Windows 95

SEQ ID NO 18
 SEQ ID NO 18

TYPE: DNA
 ORGANISM: Zea mays

NAME/KEY: unauze
 LOCATION: (164)

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 LOCATION: (351)

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 GenCode version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: November 18, 2002, 13:06:47 / search time 1334 seconds

(without alignments)
 14328.065 Million cell updates/sec

Title: US-09-857-896a-31

Perfect score: 1711

Sequence: 1 agggcgagagctctgagca.....agccaaaaaahaaaaaa 1111

Scoring table: IDENTITY, NC

Gapop 10.0, Openp 1.0

Selected: 16134066 seqs, 8091763376 residues

Total number of hits satisfying chosen parameters: 32108132

Maximum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Maximum Match 0%

Listing files: 45 summaries

Databases:

1: EST.*
 2: em_asthma.*
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 4: em_asthma.*
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 26: em_asthma.*
 27: em_asthma.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being pinned, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
1	586.2	34.3	610	11	B27602	B27602
2	585.2	34.2	700	10	B21981	B21981
3	584.6	34.2	661	11	B48242	B48242
4	584.6	34.2	661	11	B48242	B48242
5	570.6	33.3	671	13	B483019	B483019
6	569.2	33.3	667	13	B48596	B48596

7	568.6	33.2	669	13	B48375	B48375
8	553.8	32.4	637	13	B484211	B484211
9	532.8	31.1	602	13	B478020	B478020
10	493.6	28.4	669	13	B075266	B075266
11	493.6	28.4	669	13	B075266	B075266
12	476	27.8	636	13	B479219	B479219
13	465.9	26.8	605	10	B483197	B483197
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ALIGNMENTS

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 DEFINITION B27602
 ACCESSION B27602.1 GI:1016578
 KEYWORDS
 SOURCE
 ORGANISM
 Triticum aestivum
 bread wheat.
 REFERENCE
 TITLE
 AUTHORS
 JOURNAL
 COMMENT
 Expressed genes in Triticum aestivum
 (1998) (2002)
 National Institute of Genetics
 Center for Genetic Resource Information
 National Institute of Genetics
 Tel. 81-55-81-6856
 Fax. 81-55-81-6855
 Email. 81-55-81-6855
 Location: Gifu City
 1. Gifu
 /organism="Triticum aestivum"
 /db_xref="taxon:15655"


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Accession      AY545501
Version        1
Keywords       EST
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Organism       Hormum vulgare subsp. spontaneum
Reference       1. Trifolium, Hormum.
Authors        Sato, K., Saitoh, D., and Takeda, K.
Title          Bacterial ESTs sequencing project in NIG and Okayama Univ.
Comment        Contact: Saitoh, D.
                Center for Genetic Resource Information
                National Institute of Genetics
                1111 Yata, Mishima, Shizuoka 411-8540, Japan
                Tel: 81-559-81-6855
                Fax: 81-559-81-6855
                Email: tsukaguchi@nig.ac.jp.

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                        /db_xref="taxon:77009"
                        /clone="bhl2603"
                        /notes="this is an unphased cDNA library, strain H602
                        adult, heading stage top three leaves"
BASE COUNT          131 a 122 c 193 g 165 t 1 others
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Best Local Similarity 91.6% Pval: No. 4.6e-102;
Matches 614; Conservative 0; Mismatches 55; Indels 1; Gaps 1;

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Db 669 TTTCTATACACCTGCGAGCGTTCGACAGCGTTTCGACAGCGACATTTCTGCGAC 610
Oy 1078 GTTCCGACACCGCGCTGTGAAATATCTTCATATCGACATCGTCTGACATGAAAG 1137
Db 609 GTTCCGACACCGCGCTGTGAAATATCTTCATATCGACATCGTCTGACATGAAAG 550
Oy 1118 GTTCTGTGCGGCTGTGAAATATCTTCATATCGACATCGTCTGACATGAAAG 1197
Db 545 GTTCTGTGCGGCTGTGAAATATCTTCATATCGACATCGTCTGACATGAAAG 490
Oy 1158 GTTCTGTGCGGCTGTGAAATATCTTCATATCGACATCGTCTGACATGAAAG 1257
Db 489 GTTCTGTGCGGCTGTGAAATATCTTCATATCGACATCGTCTGACATGAAAG 430
Oy 1258 GGTGTTCACATGCGATACACATGCGTTCGACAGCGTTTCGACAGCGACATG 1317
Db 425 GGTGTTCACATGCGATACACATGCGTTCGACAGCGTTTCGACAGCGACATG 370
Oy 1318 GTGATGCGACATGATGACGACATGCGTTCGACAGCGTTTCGACAGCGACATG 1377
Db 365 GTGATGCGACATGATGACGACATGCGTTCGACAGCGTTTCGACAGCGACATG 310
Oy 1378 CGGATGCGACATGATGACGACATGCGTTCGACAGCGTTTCGACAGCGACATG 1437
Db 309 CGGATGCGACATGATGACGACATGCGTTCGACAGCGTTTCGACAGCGACATG 250
Oy 1438 AGCGCGCGACATGCGACATGCGTTCGACAGCGTTTCGACAGCGACATG 1497
Db 249 AGCGCGCGACATGCGACATGCGTTCGACAGCGTTTCGACAGCGACATG 190
Oy 1498 CGCGTCGCGACATGATGACGACATGCGTTCGACAGCGTTTCGACAGCGACATG 1557
Db 189 CGCGTCGCGACATGATGACGACATGCGTTCGACAGCGTTTCGACAGCGACATG 130

1598 GTTCATGCGACATGCGCGACATGCGTTCGACAGCGTTTCGACAGCGACATG 1617
Db 129 GTTCATGCGACATGCGCGACATGCGTTCGACAGCGTTTCGACAGCGACATG 70
Oy 1618 TTTCATGATATGACATGATGACATGCGTTCGACAGCGTTTCGACAGCGACATG 1677
Db 69 TTTCATGATATGACATGATGACATGCGTTCGACAGCGTTTCGACAGCGACATG 11
Oy 1678 AGATATTTT 1687
Db 10 AGATATTTT 1

RESULT 5
LOCUS      BL483013/c
DEFINITION Hormum vulgare subsp. spontaneum
            heading stage top three leaves
            cDNA clone bhl224 3', mRNA sequence.
ACCESSION  BL483013.1 GI:21161473
VERSION     BL483013.1
KEYWORDS    EST.
SOURCE      Hormum vulgare subsp. spontaneum
Organism    Hormum vulgare subsp. spontaneum
Reference    1. Trifolium, Hormum.
Authors      Sato, K., Saitoh, D., and Takeda, K.
Title        Bacterial ESTs sequencing project in NIG and Okayama Univ.
Comment      Contact: Takeda, S.
                Center for Genetic Resource Information
                National Institute of Genetics
                1111 Yata, Mishima, Shizuoka 411-8540, Japan
                Tel: 81-559-81-6855
                Fax: 81-559-81-6855
                Email: tsukaguchi@nig.ac.jp.

FEATURES
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                        /organism="Hormum vulgare subsp. spontaneum"
                        /db_xref="taxon:77009"
                        /clone="bhl2603"
                        /notes="this is an unphased cDNA library, strain H602
                        adult, heading stage top three leaves"
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Best Local Similarity 91.4% Pval: No. 4.6e-102;
Matches 615; Conservative 0; Mismatches 56; Indels 2; Gaps 1;

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Db 671 TTTCATGATATGACATGATGACATGCGTTCGACAGCGTTTCGACAGCGACATG 612
Oy 1078 GTTCCGACACCGCGCTGTGAAATATCTTCATATCGACATCGTCTGACATGAAAG 1137
Db 611 GTTCCGACACCGCGCTGTGAAATATCTTCATATCGACATCGTCTGACATGAAAG 552
Oy 1118 GTTCTGTGCGGCTGTGAAATATCTTCATATCGACATCGTCTGACATGAAAG 1197
Db 551 GTTCTGTGCGGCTGTGAAATATCTTCATATCGACATCGTCTGACATGAAAG 492
Oy 1198 GTTCTGTGCGGCTGTGAAATATCTTCATATCGACATCGTCTGACATGAAAG 1257
Db 491 GTTCTGTGCGGCTGTGAAATATCTTCATATCGACATCGTCTGACATGAAAG 432
Oy 1258 GGTGTTCACATGCGATACACATGCGTTCGACAGCGTTTCGACAGCGACATG 1317

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ACCESSION R479219
 VERSION R479219.1 GI:2157697
 KENR0000 EST
 ORGANISM Hordeum vulgare subsp. spontaneum
 Bacteria; Viridiplantae; Streptophyta; Eubryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 1 (bases 1 to 695)
 REFERENCE
 Sato, K., Sakah, D. and Takeda, K.
 Hordeum vulgare subsp. spontaneum
 Contract: Tadaea Shit-1
 Unpublished (2002)
 COMMENT
 For sequence information
 Metabolic and physiological data
 1111 Yea, Mishima, Shizuka 411-8540, Japan
 Tel.: 81-550-51-6856
 Fax: 81-550-51-6856
 Email: behn@genes.nig.ac.jp
 Location/Qualifiers
 /organism="Hordeum vulgare subsp. spontaneum"
 /strain="H602"
 /date="Mar2000 77009"
 /clone="1b-w-K. Sato unpublished cDNA library, strain H602
 multi, heading stage top three leaves"
 /db_xref="GenBank:U09857"
 /seq_start="1"
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 BASE COUNT 131 a 176 c 164 g 165 t
 ORIGIN
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 Best. Local Similarity 7.8%; Pred. No. 1.7e-83;
 Matches 434; Conservative 0; Mismatches 340; Indels 0; Gaps 0;

RESULTS 13
 AV835197
 LOCUS AV835197
 DEFINITION
 AV835197 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
 subsp. spontaneum cDNA clone Bah613, RNA sequence.
 ACCESSION AV835197 GI:14527286
 KENR0000 EST
 ORGANISM Hordeum vulgare subsp. spontaneum
 Bacteria; Viridiplantae; Streptophyta; Eubryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 1 (bases 1 to 695)
 REFERENCE
 Sato, K., Sakah, D. and Takeda, K.
 Hordeum vulgare subsp. spontaneum
 Contract: Tadaea Shit-1
 Unpublished (2001)
 COMMENT
 For sequence information
 Metabolic and physiological data
 1111 Yea, Mishima, Shizuka 411-8540, Japan
 Tel.: 81-550-51-6856
 Fax: 81-550-51-6856
 Email: behn@genes.nig.ac.jp
 Location/Qualifiers
 /organism="Hordeum vulgare subsp. spontaneum"
 /strain="H602 77009"
 /clone="Bah613"
 /date="Mar2000 77009"
 /db_xref="GenBank:U09857"
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 Best. Local Similarity 6.8%; Pred. No. 5.9e-80;
 Matches 534; Conservative 0; Mismatches 66; Indels 7; Gaps 2;

Matches 432: Conservative 0: Mismatches 28: Indels 1: Gaps 1:

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Oy 777 CAGCTTCGCCTGCTGGTGTGTGGAGATCTTCAACCCCTTCCTGTGATATGAGGAGATCG 836
Db 133 CAGCTTCGCCTGCTGGTGTGTGGAGATCTTCAACCCCTTCCTGTGATATGAGGAGATCG 192
Oy 837 CAGCTTCGCCTGCTGGTGTGTGGAGATCTTCAACCCCTTCCTGTGATATGAGGAGATCG 895
Db 193 CAGCTTCGCCTGCTGGTGTGTGGAGATCTTCAACCCCTTCCTGTGATATGAGGAGATCG 252
Oy 896 TGGAGATGATCAGTGGAGATGGGCTGGAGATCCAGAGACGGGAGAGAGAGAGAGAGAG 955
Db 253 TGGAGATGATCAGTGGAGATGGGCTGGAGATCCAGAGACGGGAGAGAGAGAGAGAGAG 312
Oy 956 GAGGCGCGGTGTGAGCCAGACAGCAAGATCTTCCTGCTCAAGCCCGACCTGGGTTC 1015
Db 313 GAGGCGCGGTGTGAGCCAGACAGCAAGATCTTCCTGCTCAAGCCCGACCTGGGTTC 372
Oy 1016 TCTTCTTCAACACCTGACACCTGTTCAGACATGCGTTGAGATGGACATTCGTGTGA 1075
Db 373 TCTTCTTCAACACCTGACACCTGTTCAGACATGCGTTGAGATGGACATTCGTGTGA 432
Oy 1076 CAGTGGACACCCCGCTTGAGAGATGCTTCAGATTCGACATCGGCTGACATGATA 1135
Db 433 CAGTGGACACCCCGCTTGAGAGATGCTTCAGATTCGACATCGGCTGACATGATA 492
Oy 1136 AGGTGCTCTGAGAGTGGCTCTGAGATCTCTGAGCTAGTACATTCCTCCCTTACG 1195
Db 493 AGGTGCTCTGAGAGTGGCTCTGAGATCTCTGAGCTAGTACATTCCTCCCTTACG 552
Oy 1196 CCGTCTGTCACACATGGGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1255
Db 553 CCGTCTGTCACACATGGGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 612
Oy 1256 A 1256
Db 613 A 613

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Search completed: November 18, 2002, 14:35:58
 300 lines : 1947 bases

GenCode version 5.1.3
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OH protein - protein search, using sw model

Run on: November 18, 2002, 14:36:08 | Search time 57 seconds

1063.027 Million cell updates/sec

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Perfect score: 2798 | I: MODERATE/PROTEIN/PSMA.....VSSALADADISDMSDFSG 534

Sequence: 1 MODERATE/PROTEIN/PSMA.....VSSALADADISDMSDFSG 534

Scoring table: BLOSUM62

Gap: 10.0, Open: 0.5

Search: 908470 seqs, 13320520 residues

Total number of hits satisfying chosen parameters: 908470

Millum DB seq length: 0

Millum DB seq length: 200000000

Post-processing: Millum Match 0%

Listing first 35 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1000	1000	1000	1000	1000
2	2777	99.7	534	20	AY269697
3	2777	99.7	534	22	AA031251
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5	2777	99.7	534	22	AA031251
6	2840	96.3	534	20	AY269698
7	2840	96.3	534	22	AA031252
8	2840	96.3	534	22	AA031252
9	2840	96.3	534	22	AA031252
10	2438	87.2	533	19	AA054443

11	1946	69.9	544	19	AA054445	Hordeum vulgare Mt.
12	1375.5	62.4	536	19	AA054444	Hordeum vulgare Mt.
13	1376.5	62.4	536	19	AA054444	Hordeum vulgare Mt.
14	1376.5	62.4	536	19	AA054444	Hordeum vulgare Mt.
15	1376.5	62.4	536	19	AA054444	Hordeum vulgare Mt.
16	1241	44.6	583	21	AA030104	Arabidopsis thaliana
17	1241	44.6	583	21	AA030104	Arabidopsis thaliana
18	1241	44.6	583	21	AA030104	Arabidopsis thaliana
19	1195	42.9	565	21	AA044052	Arabidopsis thaliana
20	1195	42.9	565	21	AA044052	Arabidopsis thaliana
21	1195	42.9	565	21	AA044052	Arabidopsis thaliana
22	1149.5	41.3	553	20	AY269722	Arabidopsis thaliana
23	1149.5	41.3	553	20	AY269722	Arabidopsis thaliana
24	1149.5	41.3	553	20	AY269722	Arabidopsis thaliana
25	1085.5	39.0	511	21	AA033599	Arabidopsis thaliana
26	1085.5	39.0	511	21	AA033599	Arabidopsis thaliana
27	1085.5	39.0	511	21	AA033599	Arabidopsis thaliana
28	983	35.4	430	21	AA033705	Arabidopsis thaliana
29	982	34.6	506	21	AA001793	Soybean Mt homo
30	918	34.4	187	21	AA001794	Soybean Mt homo
31	918	34.4	187	21	AA001794	Soybean Mt homo
32	927.5	33.5	526	22	AA031555	Arabidopsis thaliana
33	927.5	33.5	526	22	AA031555	Arabidopsis thaliana
34	927.5	33.5	526	22	AA031555	Arabidopsis thaliana
35	901	32.4	450	21	AA001798	Wheat Mt homo
36	882	31.9	452	20	AA014135	Wheat Mt homo
37	786.5	28.6	496	21	AA044822	Maize disease resist
38	786.5	28.6	496	21	AA044822	Maize disease resist
39	786.5	28.6	496	21	AA044822	Maize disease resist
40	786.5	28.6	496	21	AA044822	Maize disease resist
41	745.5	26.8	464	20	AA044601	Maize Mt1 protein
42	745.5	26.8	464	20	AA044601	Maize Mt1 protein
43	745.5	26.8	464	20	AA044601	Maize Mt1 protein
44	745.5	26.8	464	20	AA044601	Maize Mt1 protein
45	735	26.4	509	21	AA044603	Maize Mt1 protein

ALIGNMENTS

RESULT 1	AA001805	standard	Protein: 534 AA.
ID	AA001805		
1	27-OCT-2000	(first entry)	
2	AA001805		
3	Wheat Mt1 homologue; putative protein sequence 14.		
4	Wheat: Mt1 homologue; disease resistance.		
5	Triticum aestivum.		
6	W000003110-42.		
7	22-OCT-2000.		
8	17-DEC-1998.	99M-0330181.	
9	18-DEC-1998.	98M5-012737.	
10	(copy) DJ PONT DE HENOURS & CO E. I.		
11	Canham RE, Miao G, Rafalski JN, Fang Y, Sakai H, Taramino G.		
12	WPI: 2000-43159/37.		
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Oy 215 SPTWVOTGILACQCTANLUS--UNKEKFPWYTRSRMEOFPYVVOGISTPLACQALTEP 272
Db 248 SVTKVDIALNRGTJNHRFQONSRSPDRKXIOSLEKDKVTEISPIVTHFVAVLEL 307
Oy 273 LIDIGIGLWISPRVYILLCQTKLMIEMALETODASVIGQAVVSRNNEFPW 332
Db 308 THSTGLASTLAMPPEPLVYLLVSTKLEVIITKGLATIDCKOVCVRECAVVOGDDLENF 367
Oy 333 HRPDVLFFTHLTQONATQNAHVVTVCCLAKCTNMHIGLAIKXVILALQFTCSY 392
Db 368 GQKPEIIEJLHVLVTHQDLPFNKSTIERKMNCTHSTKQVYELHLYQAVOLDSY 427
Oy 393 ITPPLVATVQCSNMKNSIFBQTNALTNHNTKKEKRVBTQMLAQMGIDATPSH 452
Db 428 VYLDKLVATQCSNMKSTVYDSVVALKKNHRTMKT-----KGRHSSTPFS 480
Oy 453 GTSPPSRASSPVHLLKMGKSDQDSAPSPH 486
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Search completed: November 18, 2002, 15:36:05
 Job Time : 68 secs


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: SOFTWARE: Microsoft Windows 95
: SEQ ID NO 14
: LENGTH: 114
: TYPE: PRT
: FEATURES: see mays
US-09-183-959-14

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Matches 85; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

OR 323 VERSKMFHFRNPPWAFVTLTFLQVNAQMAHYVAVTQDLKQFFHMGICISIMVTVL 392
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DB 1 VPSDQHFHFRNPPWAFVTLTFLQVNAQMAHYVAVTQDLKQFFHMGICISIMVTVL 60

OR 383 GLALQFCSTFFPLALVYQNSMKSISFDQGTAKALTNMTRNAKKKKVVD 436
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DB 61 GLALQFCSTFFPLALVYQNSMKSISFDQGTAKALTNMTRNAKKKKVVD 114

RESULT 10
US-09-183-959-4
: Sequence 4, Application US/09183959
: Patent No. 5858713
: GENERAL INFORMATION:
: APPLICANT: Caprom, Rebecca E.
: INVENTOR: Caprom, Rebecca E.
: APPLICANT: MNO, Qao-Hua Anzoni
: INVENTOR: MNO, Qao-Hua Anzoni
: APPLICANT: Tashino, Graziana
: TITLE OF INVENTION: COIN DNA ENCODING SOUTHERN LAMP BLIGHT RESISTANCE
: CURRENT APPLICATION NUMBER: US/09/183,959
: CURRENT FILING DATE: 1998-11-02/04,439
: EARLIER FILING DATE: NO/09/03/26number 5, 1997
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Microsoft Windows 95
: LENGTH: 80
: TYPE: PRT
: FEATURES: see mays
US-09-183-959-4

Query Match
Beat Local Similarity 5.7%: Score 187; DB 4; Length 80;
Matches 39; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

OR 232 HCSMSGKPYHYKRGMDYVVCISGALQVLTLEDDGQCTGTFSTFVAT 291
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DB 1 HYPKQDTHFRNPPWAFVTLTFLQVNAQMAHYVAVTQDLKQFFHMGICISIMVTVL 60

OR 292 LCCGCTHETIMTMALE 309
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DB 61 LCCGCTHETIMTMALE 78

RESULT 11
US-09-183-959-6
: Sequence 6, Application US/09183959
: Patent No. 6103332
: GENERAL INFORMATION:
: APPLICANT: Caprom, Rebecca E.
: INVENTOR: Caprom, Rebecca E.
: APPLICANT: MNO, Qao-Hua Anzoni
: INVENTOR: MNO, Qao-Hua Anzoni
: APPLICANT: Tashino, Graziana
: TITLE OF INVENTION: COIN DNA ENCODING SOUTHERN LAMP BLIGHT RESISTANCE
: FILE REFERENCE: BB-1125
: CURRENT FILING DATE: 1998-11-02/09/183,959
: EARLIER FILING DATE: 1998-11-02/04,439
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Microsoft Windows 95

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: SEQ ID NO 6
: LENGTH: 52
: TYPE: PRT
: FEATURES: see mays
US-09-183-959-6

Query Match
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Matches 24; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

OR 384 LALALGCTFFPLALVYQNSMKSISFDQGTAKALTNMTRNAKKKKVVD 435
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DB 1 VVILGCTFFPLALVYQNSMKSISFDQGTAKALTNMTRNAKKKKVVD 52

RESULT 12
US-08-868-793-4
: Sequence 11, Application US/08808793
: Patent No. 5858713
: GENERAL INFORMATION:
: APPLICANT: Sordeland, David K.
: INVENTOR: Sordeland, David K.
: APPLICANT: MNO, Qao-Hua Anzoni
: INVENTOR: MNO, Qao-Hua Anzoni
: APPLICANT: Tashino, Graziana
: TITLE OF INVENTION: AND USE THEREOF
: CORRESPONDENCE ADDRESS:
: ADDRESS: Nixon, Barjave, Devans & Doyle LLP
: CITY: Rochester
: STATE: New York
: COUNTRY: USA
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release 41.0, Version 41.30
: APPLICATION NUMBER: US/08/808,793
: FILING DATE:
: CLASSIFICATION: 435
: PRIORITY DATE:
: APPLICATION NUMBER: US 60/031,361
: FILING DATE: 24-DEC-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/012,649
: FILING DATE: 01-MAR-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Graham, Susan J.; 103
: TELEPHONE: 716-563-1400
: TELEFAX: 716-563-1400
: INFORMATION FOR SEQ ID NO: 4:
: SOURCE: CHARACTERISTICS:
: TYPE: amino acid
: STANDARDS: not relevant
: MOLECULE TYPE: protein
US-08-868-793-4

Query Match
Beat Local Similarity 3.5%: Score 96.5; DB 2; Length 2104;
Matches 44; Conservative 34; Mismatches 89; Indels 31; Gaps 7;
346 LQNNFQMAHYVAVTQDLKQFFHMGICISIMVTVLGLALQFCSTFFPLALVYQNSMKSISFDQGTAKALTNMTRNAKKKKVVD 405

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463 SPW-----LHKGCRSDPOGATSPPTMEKADWPPVYVWRLNADDERBSV 516
 482 SPYSCISYELVGEKGDONNENKISVSESVSYTORPATTMAYKRVKS 541
 517 SSALADIDRANDEFSG 534
 542 TTSI--SLRSPFRLNG 557

DB 542 TTSI--SLRSPFRLNG 557
 Search completed: November 18, 2002, 15:40:24
 Job time : 27 secs

RESUME 15
 US-09-857-896a-32-512A-3
 ? Sequence 3, Application US/0872512A
 ? Patent No. 6023705
 ? INVENTOR: Soderlund, David M.
 ? APPLICANT: Knipole, Douglas C.
 ? APPLICANT: Knipole, Douglas C.
 ? TITLE OF INVENTION: RESISTANT CHANNELS FROM
 ? TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE
 ? NUMBER OF INVENTOR: 3
 ? NUMBER OF INVENTOR: 3
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: NIXON, HANNAVE, DEVANS & DOYLE LLP
 ? CITY: Rochester
 ? STATE: New York
 ? COUNTRY: USA
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: floppy disk
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Patent Release #1.0, Version #1.30
 ? APPLICATION NUMBER: 06/08772.512A
 ? FILING DATE:
 ? CLASSIFICATION: 435
 ? PRIORITY REFERENCE: 435
 ? APPLICATION NUMBER: US 08/608,518
 ? FILING DATE: 01-MAY-1996
 ? NAME/INVENTOR: Soderlund, David M.
 ? REGISTRATION NUMBER: 34,103
 ? REFERENCE/DOCKET NUMBER: 35603/601(CRD-1657)
 ? TELEPHONE: 716-263-1600
 ? TELEFAX: 716-263-1600
 ? IMPRESSION: 35603/601(CRD-1657)
 ? SEQUENCE CHARACTERISTICS: 3:
 ? LENGTH: 2105 amino acids
 ? STRATEGIC: 3:
 ? STRATEGY: 3:
 ? TOPOLOGY: linear
 ? MOLECULAR TYPE: protein
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 382 LVGVLDAG-PM-----HHFFVITFD-----SYVLAIVAMRY 421
 406 SSKMSSTFPGDA--KALNNKATAEK-KYVGGDKMLMONGATSPGSPGDA 452
 422 DELQKAEERBAERARIVREMAAAKALEPAAVMAADQADAAALALPBAK 481
 463 SPW-----LHKGCRSDPOGATSPPTMEKADWPPVYVWRLNADDERBSV 516
 482 SPYSCISYELVGEKGDONNENKISVSESVSYTORPATTMAYKRVKS 541
 517 SSALADIDRANDEFSG 534

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GenScore version 5.1.3
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OK protein - protein search, using sw model

Run on: November 18, 2002, 15:38:38 | Search time 14 seconds

336,545 Million cell updates/sec

Title: US-09-637-696a-32

Sequence: 2784

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 15 summaries

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26	89.5	3.0	145	US-09-855-637-22	Sequence 12, App1
27	89.5	3.0	145	US-09-855-637-22	Sequence 12, App1
28	89.5	3.0	145	US-09-855-637-22	Sequence 12, App1
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39	89.5	3.0	145	US-09-855-637-22	Sequence 12, App1
40	89.5	3.0	145	US-09-855-637-22	Sequence 12, App1
41	89.5	3.0	145	US-09-855-637-22	Sequence 12, App1
42	89.5	3.0	145	US-09-855-637-22	Sequence 12, App1
43	89.5	3.0	145	US-09-855-637-22	Sequence 12, App1
44	89.5	3.0	145	US-09-855-637-22	Sequence 12, App1
45	89.5	3.0	145	US-09-855-637-22	Sequence 12, App1

ALIGNMENTS

1	US-10-029-001-9	Sequence 1	US-10-029-001-9	Sequence 1
2	US-10-029-001-9	Sequence 1	US-10-029-001-9	Sequence 1
3	US-10-029-001-9	Sequence 1	US-10-029-001-9	Sequence 1
4	US-10-029-001-9	Sequence 1	US-10-029-001-9	Sequence 1
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6	US-10-029-001-9	Sequence 1	US-10-029-001-9	Sequence 1
7	US-10-029-001-9	Sequence 1	US-10-029-001-9	Sequence 1
8	US-10-029-001-9	Sequence 1	US-10-029-001-9	Sequence 1
9	US-10-029-001-9	Sequence 1	US-10-029-001-9	Sequence 1
10	US-10-029-001-9	Sequence 1	US-10-029-001-9	Sequence 1
11	US-10-029-001-9	Sequence 1	US-10-029-001-9	Sequence 1
12	US-10-029-001-9	Sequence 1	US-10-029-001-9	Sequence 1
13	US-10-029-001-9	Sequence 1	US-10-029-001-9	Sequence 1
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15	US-10-029-001-9	Sequence 1	US-10-029-001-9	Sequence 1
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27	US-10-029-001-9	Sequence 1	US-10-029-001-9	Sequence 1
28	US-10-029-001-9	Sequence 1	US-10-029-001-9	Sequence 1
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33	US-10-029-001-9	Sequence 1	US-10-029-001-9	Sequence 1
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45	US-10-029-001-9	Sequence 1	US-10-029-001-9	Sequence 1

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0Y 210 NMLSHNSKFGHNYKRNKSDFFVWVIGISPLKMCVALITLFDIDIGLTVLWSTP- 289
0Y 216 OMFSPGKQFHTL-----LIVLWVDFPGLKMLTGYVLTIDGSGFT- 290
0Y 290 VILLCWCEFLMNLINSEALIDGASVYKCAVPESNKKF--FHEWOWLEFHLIF- 347
0Y 281 -----GVDC-----KHQJLAKHNRHMMHITWVATLCPH-----ITFLMLVIT 395
0Y 348 Q-----NMQDQLENY-----WATPOLKCEKCHMGLGCSKPKVGLALAPCESTP 394
0Y 326 QOLNMYTDOOYASLP-MLNSTWVPIYOLKAPFAGKSK-----NFM-CPH 378
0Y 378 VASDTELEKTHFRHNSKSTYTHESHTWVDFPDLGTTSSSKK----- 428
0Y 446 CDATP-----SNGSPKSPKSSPVMLKHKCNDSODQAPFSP--FHEWED 493
0Y 429 -ATPDPSPNOCJRNKSNASNSPISSTVSVOTSDQELAPDEKMLGOLN 495

RESULT 3
US-09-750-143-879
Sequence 879, Application US/0975143
PATENT NO. US2002002248A1
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: McChesney, Jennifer L.
APPLICANT: Fenger, Gary R.
APPLICANT: Jiaeng, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Fenger, Gary R.
APPLICANT: Fenger, Gary R.
APPLICANT: Day, Craig H.
APPLICANT: Vedelick, Thomas S.
APPLICANT: Vedelick, David L.
APPLICANT: Wang, Aljun
APPLICANT: Shenley, Yaelit A.M.
APPLICANT: Wang, Aljun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 334
SOFTWARE: Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
ORGANISM: Homo sapiens

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Matches 36; Conservative 54; Mismatches 114; Indels 92; Gaps 13;
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0Y 52 ADEBCEBQSDGDELFQPHMLPDKTANLHGVLTLLHRYTLHNSKQGTFTKTP- 111
0Y 52 NMLAALKETKMLGKMGISPLAVTDPISGCSKSPKSNDRKSPKSSKXK- 110
0Y 112 LVNKVPMVSTITLAVLTPVATLAVQVNG-----TKKK 149
0Y 111 -----DTKCKGKSNKSGSLQHTITPLVAVNTTSV--TNALSKLDRKHK 163
0Y 110 -----DTKCKGKSNKSGSLQHTITPLVAVNTTSV--TNALSKLDRKHK 163
0Y 111 FPMHDMMLKQKGLS-----FPMVATLSTSPHRSSTKYLMLNMO 198

RESULT 3
US-09-750-143-879
Sequence 879, Application US/0975143
PATENT NO. US2002002248A1
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: McChesney, Jennifer L.
APPLICANT: Fenger, Gary R.
APPLICANT: Jiaeng, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Fenger, Gary R.
APPLICANT: Day, Craig H.
APPLICANT: Vedelick, Thomas S.
APPLICANT: Vedelick, David L.
APPLICANT: Wang, Aljun
APPLICANT: Shenley, Yaelit A.M.
APPLICANT: Wang, Aljun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 334
SOFTWARE: Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
ORGANISM: Homo sapiens

Query Match
Beat Local Similarity 3.3%; Score 92; DB 10; Length 339;
Matches 36; Conservative 54; Mismatches 114; Indels 92; Gaps 13;
0Y 2 ADEYTPP--ARTPEPSP--AAVLPVWVWVSLNHLMLG--HFKRKHK 51
0Y 52 ADEBCEBQSDGDELFQPHMLPDKTANLHGVLTLLHRYTLHNSKQGTFTKTP- 111
0Y 52 NMLAALKETKMLGKMGISPLAVTDPISGCSKSPKSNDRKSPKSSKXK- 110
0Y 112 LVNKVPMVSTITLAVLTPVATLAVQVNG-----TKKK 149
0Y 111 -----DTKCKGKSNKSGSLQHTITPLVAVNTTSV--TNALSKLDRKHK 163
0Y 110 -----DTKCKGKSNKSGSLQHTITPLVAVNTTSV--TNALSKLDRKHK 163
0Y 111 FPMHDMMLKQKGLS-----FPMVATLSTSPHRSSTKYLMLNMO 198
0Y 164 ETEVSLKTFQPDNDAPRFTQSTV-----KRLGSLSTPGL-----RMYAFRPGFNS 215
0Y 199 QVQCKMKNLHNDHNMENYVSLGATLALVATSPVSDSLN-----REFMT 253
0Y 216 YTVYVLTLDQFPMALNSKRDYKYSKSDPPVWVIGISPLKMCVALITLFDI 275
0Y 254 GSKALISLTLSTLHML-----TKMKNI-----DLQKWTFTPLNAY----- 285
0Y 276 DQGLTGLMSTPPTL 293
0Y 296 -----SDEAVLL 303

RESULT 3
US-09-760-669-979
Sequence 879, Application US/0976069
PATENT NO. US2002002248A1
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: McChesney, Jennifer L.
APPLICANT: Fenger, Gary R.
APPLICANT: Jiaeng, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Fenger, Gary R.
APPLICANT: Day, Craig H.
APPLICANT: Vedelick, Thomas S.
APPLICANT: Vedelick, David L.
APPLICANT: Wang, Aljun
APPLICANT: Shenley, Yaelit A.M.
APPLICANT: Wang, Aljun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
CURRENT APPLICATION NUMBER: US/09/760,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 334
SOFTWARE: Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
ORGANISM: Homo sapiens

Query Match
Beat Local Similarity 3.3%; Score 92; DB 10; Length 339;
Matches 36; Conservative 54; Mismatches 114; Indels 92; Gaps 13;
0Y 2 ADEYTPP--ARTPEPSP--AAVLPVWVWVSLNHLMLG--HFKRKHK 51
0Y 52 ADEBCEBQSDGDELFQPHMLPDKTANLHGVLTLLHRYTLHNSKQGTFTKTP- 111
0Y 52 NMLAALKETKMLGKMGISPLAVTDPISGCSKSPKSNDRKSPKSSKXK- 110
0Y 112 LVNKVPMVSTITLAVLTPVATLAVQVNG-----TKKK 149
0Y 111 -----DTKCKGKSNKSGSLQHTITPLVAVNTTSV--TNALSKLDRKHK 163
0Y 110 -----DTKCKGKSNKSGSLQHTITPLVAVNTTSV--TNALSKLDRKHK 163
0Y 111 FPMHDMMLKQKGLS-----FPMVATLSTSPHRSSTKYLMLNMO 198
0Y 164 ETEVSLKTFQPDNDAPRFTQSTV-----KRLGSLSTPGL-----RMYAFRPGFNS 215
0Y 199 QVQCKMKNLHNDHNMENYVSLGATLALVATSPVSDSLN-----REFMT 253
0Y 216 YTVYVLTLDQFPMALNSKRDYKYSKSDPPVWVIGISPLKMCVALITLFDI 275
0Y 254 GSKALISLTLSTLHML-----TKMKNI-----DLQKWTFTPLNAY----- 285
0Y 276 DQGLTGLMSTPPTL 293
0Y 296 -----SDEAVLL 303

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```

!! OCKANISB. mus musculus
US-09-857-369.31
Query Match: 3184; Score: 83.5; DB: 10; Length: 364;
Accession: U00001.1; E-value: 2.2e-14;
Matches: 33; Conservative: 40; Mismatches: 85; Indels: 69; Gaps: 14;

Oy 256 VVLSLPLACVALLTLDLDTGCTANSTFVYL-LVYQKLENIIMBALEIGDA 314
Db 49 VLNGLVNVADGPRKH-----TVTSLNLAADCTSTLPTI-----A 91
Oy 315 SYTKA--PIVRSNKEPRNRPDRIPLFTIKELQANDQA-----HWYVA 361
Db 92 SRYWGNRP-----RGR-MKEPTVYDLENLSVPLALADRCICVAPVA-- 141
Oy 362 TRELKCTRNHIGLSIKVIALDLTLCST--TFPLALVY----QMSNKRSTED 415
Db 142 -----QNHRTVSLAKV--LIVVLDNLELLPLVILNLTVPNSLDGACTED- 390
Oy 416 GTAKALNNNTNKKKKVYEDID---LMDQNGCATPSGCTSPWSPASSVYALNG 471
Db 191 -----SRYTKDPRVAKVNVPLVYVGIIVFIDGSDNSVIALGELITVIR-- 243
Oy 472 MRSDDP 478
Db 244 LKSSRP 250

Search completed: November 18, 2002, 15:47:00
Job time: 36 secs

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[illegible][illegible]

GenCore version 5.1.3
Copyright (c) 1995 - 2002 Comugen Ltd.

OM protein - nucleic search, using frame_plus.g2n model

Run on: November 18, 2002, 15:39:43 | Search time 232 seconds

(without alignments) 4772.092 Million cell updates/sec

Title: US-09-857-896a-32

Reference score: 7784

Sequence: 1 MGVRYFNRATVPTFRPM.....VSSADMDPFRMDSPR 534

Scoring table:

BLOSUM62 0.0 Xmatch 0.5

Gapop 10.0 - Gapext 0.5

Delop 6.0 - Delact 7.0

Searched: 218539 seqs, 11595959 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length 0

Maximum DB seq length 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Library size 49 summaries

Command line parameters: -pmy-1h

-O/-S/2/USFR0.spool/US0807896/runs_14112002.091117.13845/APP_query_frame_1.711

-DBs-Geneseq-101002 -OPTM-fastap -SUPIX-rng -MINMATCH-0.1 -LOCAL-0

-USF-45 -DOCCUCLIS-200 -TMR-SCORE-PC -TMR-MAX-0.000000 -TMR-MIN-0.000000

-HDS-LOCAL -OUTPRG-pro -NOM-ext -HDSIZE-500 -MINLEN-0 -MAXLEN-200000000

-NO-CLUSTER-0 -NO-CLUSTER-1 -FRAMES-1112002.091117.1385 -MCHP-6 -ICPV-3

-MANY-IMDWT-30 -THRAUS-1 -XNAPR-10 -XNAPR-0.5 -FDRAP-6 -FDRAP-7

-GAPOP-10 -YAPEXT-0.5 -DELAP-6 -DELACT-7

Database:

1: /S1D52/gcdata/geneseq/geneseq-emb/NA1380.DMT*

2: /S1D52/gcdata/geneseq/geneseq-emb/NA1381.DMT*

3: /S1D52/gcdata/geneseq/geneseq-emb/NA1382.DMT*

4: /S1D52/gcdata/geneseq/geneseq-emb/NA1383.DMT*

5: /S1D52/gcdata/geneseq/geneseq-emb/NA1384.DMT*

6: /S1D52/gcdata/geneseq/geneseq-emb/NA1385.DMT*

7: /S1D52/gcdata/geneseq/geneseq-emb/NA1386.DMT*

8: /S1D52/gcdata/geneseq/geneseq-emb/NA1387.DMT*

9: /S1D52/gcdata/geneseq/geneseq-emb/NA1388.DMT*

10: /S1D52/gcdata/geneseq/geneseq-emb/NA1389.DMT*

Result	Score	Query	Length	DB	ID	Description
1	2784	100.0	1711	21	AAAS5715	Wheat M10 homologue
2	2777	99.7	1693	22	AAAS5716	Nucleotide sequence
3	2740	98.4	1868	20	AAAS3049	Wheat M10 fungal r
4	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
5	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
6	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
7	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
8	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
9	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
10	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
11	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
12	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
13	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
14	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
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16	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
17	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
18	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
19	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
20	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
21	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
22	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
23	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
24	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
25	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
26	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
27	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
28	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
29	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
30	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
31	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
32	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
33	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
34	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
35	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
36	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
37	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
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39	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
40	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
41	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
42	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
43	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
44	2680	96.3	1868	20	AAAS3049	Nucleotide sequence
45	2680	96.3	1868	20	AAAS3049	Nucleotide sequence

ALIGNMENTS

RESULT 1

AAAS5715 standard; GDNV, 1711 BP.

AAAS5715:

27-OCT-2000 (first entry)

Wheat M10 homologue putative coding sequence #4.

Wheat M10 homologue: disease resistance; ss.

Tricolum aestivum.

Key

Location/Qualifiers

1..1005

/product= 'M10 homologue'

and is derived by analysis of the total score distribution.

XX M0200056110-A2.
 XX 22-JUN-2000.
 XX 17-DEC-1999: 9960-0630181.
 XX 18-DEC-1998: 9608-01117277.
 XX (P00) J DU POIT DE NORDON & CO E I.
 XX Cahoon RE, Miao G, Rafalski JM, Fang Y, Sakai H, Taramino G:
 WPE: 2006-4-13156/37.
 XX P50801-06080105.
 XX New polynucleotide encoding a Mlo homologue polypeptide, useful for
 XX creating transgenic plants with altered levels of disease resistance -
 XX Claim 2: Page 64: 79p: English.
 XX The present sequence is a putative coding sequence for a Mlo homologue
 XX from wheat. It was identified by searching a root and leaf cDNA library
 XX for sequences encoding proteins similar to Mlo from hordeum vulgare
 XX (hordeum vulgare L.). The protein encoded by this sequence is not present in
 XX cereals (i. sp. hordeum upon the plant, and its inactivation leads to the
 XX pruning of disease resistance even if the pathogen is not present. The
 XX increased disease resistance, as well as allowing researchers to find
 XX other resistance conferring genes and proteins.
 XX Sequence 1711 BP: 377 A: 505 C: 473 G: 356 T: 0 other:
 50
 Alignment Scores:
 Seq No: 2,266-374 Length: 1711
 Score: 2784.00 Matches: 534
 Percent similarity: 100.00% Conservative: 0
 Percent dissimilarity: 100.00% Indels: 0
 Query Match: 21 Gaps: 0
 US-09-857-896a-32 (1-594) x AA65715 (1-1711)
 0y 1 MetAlaGluAspArgTrpGlnProPheLysThrGlyAsnProThrProSerTrpAla 20
 0y 1 ATGCGCGAGGCTGCAAGATGACGCGCGCGGAGACGCGCGCGAGCGCGCGCGCGCG 60
 0y 21 ValAlaLeuValProAlaValMetAlaLeuValSerValLeuLeuGluValAlaLeuVal 40
 0y 61 GAGGCGGCTGCTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
 0y 41 GylGluGluValSerPheMetAlaGlyGlyAlaGluValAlaGluValAlaGluVal 60
 0y 121 AGGCG 180
 0y 61 TleGluAlaGluValMetLeuValGluValSerValLeuLeuValValThrAlaAsp 80
 0y 181 ATGAGCGAGGCG 140
 0y 81 ProTlSerGluTrpLeuGly11SerGluValAlaAlaSerTlMetAlaProGluSerGlu 100
 0y 241 CGATGCG 200
 0y 101 ProGluGluSerValGluSerLysArgTrpGlnAlaTrpGluValGluValGluVal 120
 0y 301 CG 160
 0y 121 SerGluMetSerGluTrpGluGluValGluValGluValGluValGluValGluVal 140
 0y 351 TCGCTGATGATGCGGCGAGGCTGCGACGCTGCGACGCGCGCGCGCGCGCGCGCGCG 200
 0y 141 PheAlaValThrGluTrpGluGluValGluValGluValGluValGluValGluVal 160
 421 TTCGATGTCACCTGACAGCGCATGATACAGGCGCTGACGCGCGTCCAAATGAGAGACGCG 480
 0y 161 LysArgTrpGluTrpThrAlaLysLeuGluTrpGluProMetAlaMetArgAlaGlu 180
 0y 481 AGAGAGAGGAG 540
 0y 181 PheArgPheMetAlaSerTlSerPheValGluValGluValGluValGluValGluVal 200
 0y 541 TTCG 600
 0y 201 GylTleSerGluTrpValAlaPhePheGluGluValPhePheSerValThrValGluVal 220
 0y 601 GSCGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 460
 0y 221 TyrLeuThrMetAlaGluAlaPheAlaValMetAlaLysAlaSerGluValPheArg 240
 0y 661 TACG 720
 0y 241 PheAlaValGlyTlLeuArgGluMetGluArgPheGluValValValGluValSer 260
 0y 721 TleArgGluTrpGluValGluValGluValGluValGluValGluValGluValGluVal 780
 0y 261 LysArgGluTrpGluValAlaLysArgTrpGluValGluValGluValGluValGluVal 280
 0y 781 CG 840
 0y 281 LeuArgTrpLysPhePheArgGluValTleLeuGluGluValGluValGluValGluVal 300
 0y 841 CGACGCGGATGTTTCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 0y 301 MetTleLeuGluGluValGluValGluValGluValGluValGluValGluValGluVal 320
 0y 901 ATGATGCTGTGAG 960
 0y 321 ProValValGluProSerMetLysPheMetArgPheMetArgProArgTrpValLeuPhe 340
 0y 961 CG 1020
 0y 341 PheAlaLysArgTrpLeuPheGluAlaPheGluTlMetAlaLysPheValTrpThrVal 360
 0y 1021 TCG 1080
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 0y 1081 GCG 1140
 0y 381 ValGluGluValAlaGluTlPheGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 400
 0y 1141 GTGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 0y 401 GylValThrGluValSerPheMetArgGluSerTlPheArgPheGluTlGluAlaValAla 420
 0y 1201 GCGCGCGAGTGGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1260
 0y 421 LeuThrArgTrpAlaGluThrAlaValGluValGluValGluValGluValGluVal 1320
 0y 1261 GTGCGCGAGTGGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1380
 0y 441 MetAlaLysMetTleGluSerAlaTrpProSerAlaGluTrpSerProMetProSerArg 460
 0y 1381 GGTGCG 1440
 0y 461 AlaSerSerProValGluValMetAlaLysValGluValGluValGluValGluVal 480
 0y 1441 GCGCGCGAGTGGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1500
 0y 501 LysArgTrpAlaLysGluArgPheAlaArgPheValGluValGluValGluValGluVal 520
 0y 1501 CATCGCGCGAGTGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560

[illegible]

Tue Nov 19 14:16:04 2002

us-09-857-896a-32.rn1

Page 6

[illegible][illegible]

Tue Nov 19 14:16:04 2002

us-09-857-896a-32.rn1

Page 10

[illegible][illegible]

Tue Nov 19 14:16:04 2002

us-09-857-896a-32.rnpb

Page 6

1 PRIOR APPLICATION NUMBER: US 60/284,647
2 PRIOR FILING DATE: 2001-01-16
3 PRIOR APPLICATION NUMBER: US 60/300,111
4 PRIOR FILING DATE: 2001-06-22
5 NUMBER OF SEQ ID NOS: 579
6 SEQ ID NO: 236
7 LENGTH: 1491
8 TYPE: DNA
9 ORGANISM: Arabidopsis thaliana
10 US-08-09368-12368

[illegible]

Tue Nov 19 14:16:04 2002

us-09-857-896a-32.rnpb

Page 12

[illegible]

Search completed: November 18, 2002, 18:08:40
Job time : 75 secs

GenScore version 3.1.3
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OM protein - protein search, using SW method

Run on: November 18, 2002, 15:35:13 / Search time 43 seconds

Title: US-09-857-896a-32 (Without alignments) 1193,853 Million call updates/sec

Perfect score: 7794

Sequence: 1 MVDGYPRHTVPTFRFNM.....VSSALMDVPSMDTSFGS 534

Scoring table: BLOSUM62, gapop 10.0, gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 9

Maximum DB seq length: 500000000

Post-processing: Minimum Match 0%

Listing first 40 summaries

Database:

1: PIR_3.1
2: PIR_2
3: PIR_1
4: PIR_0

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2434	87.4	533	2	Mio protein - bart
2	1960	70.4	544	2	probable mio protein - b
3	1276.2	63.3	537	2	H-virus protein - b
4	1246.5	44.8	570	2	hypothetical protein
5	1144	44.6	583	2	hypothetical protein
6	1106	39.7	572	2	similar to Mio pro
7	1068	38.4	580	2	hypothetical protein
8	1068	38.4	580	2	hypothetical protein
9	955	34.3	466	2	hypothetical protein
10	923.5	33.5	528	2	hypothetical protein
11	898.5	30.3	428	2	hypothetical protein
12	898.5	30.3	428	2	hypothetical protein
13	898.5	30.3	428	2	hypothetical protein
14	898.5	30.3	428	2	hypothetical protein
15	898.5	30.3	428	2	hypothetical protein
16	898.5	30.3	428	2	hypothetical protein
17	898.5	30.3	428	2	hypothetical protein
18	898.5	30.3	428	2	hypothetical protein
19	898.5	30.3	428	2	hypothetical protein
20	898.5	30.3	428	2	hypothetical protein
21	898.5	30.3	428	2	hypothetical protein
22	898.5	30.3	428	2	hypothetical protein
23	898.5	30.3	428	2	hypothetical protein
24	898.5	30.3	428	2	hypothetical protein
25	898.5	30.3	428	2	hypothetical protein
26	898.5	30.3	428	2	hypothetical protein
27	898.5	30.3	428	2	hypothetical protein
28	898.5	30.3	428	2	hypothetical protein
29	898.5	30.3	428	2	hypothetical protein

30	95	3.4	250	2	C97013	AAC-type sporidial
31	94.5	3.4	475	2	C69587	protein 609PU.4 (
32	94.5	3.4	489	2	B33416	nuclear factor 1
33	94.5	3.4	506	2	A33416	nuclear factor 1
34	94.5	3.4	506	2	A33416	nuclear factor 1
35	94.5	3.4	510	2	B71695	hypothetical protein
36	94.5	3.4	510	2	B71695	hypothetical protein
37	94.5	3.4	510	2	B71695	hypothetical protein
38	94.5	3.4	510	2	B71695	hypothetical protein
39	94.5	3.4	510	2	B71695	hypothetical protein
40	94.5	3.4	510	2	B71695	hypothetical protein
41	94.5	3.4	510	2	B71695	hypothetical protein
42	94.5	3.4	510	2	B71695	hypothetical protein
43	94.5	3.4	510	2	B71695	hypothetical protein
44	94.5	3.4	510	2	B71695	hypothetical protein
45	94.5	3.4	510	2	B71695	hypothetical protein

ALIGNED

RESULT 1

T04463 - barley

C:barley - non-reducing (barley)

C:barley - non-reducing (barley)

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C:barley - non-reducing (barley)

C:barley - non-reducing (barley)

C:barley - non-reducing (barley)

Db 134 AADP07.....VATSLMAYDQITTEFLANPHTVATLNNQDAIKMKNWED 166
 11
 Db 166 EYSLSELPQANDAPRDTQTSYVNM-GLSTGCMNVAVFPQPSRYVXVITL 224
 Db 187 EYIN EDDMDQSPFRLDIEHSYVBNMNAHNFYQVCFPQDILSVKSYL 245
 Db 225 RAGSTNLSINSPDPTQYRKMDFQYVQVQVQVQVQVQVQVQVQVQV 264
 11
 Db 246 RRGVSTVLAADKPEFQVYKSLSDDFYVQVQVQVQVQVQVQVQVQV 305
 Db 285 SFPTVLAADKPEFQVYKSLSDDFYVQVQVQVQVQVQVQVQVQV 344
 11
 Db 306 TAPFVLAADKPEFQVYKSLSDDFYVQVQVQVQVQVQVQVQVQV 365
 Db 345 TLPDQVMAVQVYVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 404
 Db 366 VLDQVY.....QVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 433
 Db 405 GSNMKSIFDQVYVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 433
 Db 414 GSNMKSIFDQVYVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 442

RESULT 11

H. vulgare M10 protein homology A12944110 [imported] - Arabidopsis thaliana

T00691

C-Species: Arabidopsis thaliana (model-ear cross)

C-Date: 01-Feb-1999 Sequence-Revision 12-Feb-1999 tseq-Change 15-Jun-2001

R-Name: A12944110, S.D. Lau, S.J. Lin, X. K. Kitchin, K.A. Croxby, M.L. Brandon, R.C. Sykes,

submitted to the EMBL data library, June 1998

A-Description: Arabidopsis thaliana chromosome II BAC F6B3 genomic sequence.

A-Accession: T00691 414480

A-Status: translated from cDNA/EMBL/DBD

A-Status: translated from cDNA/EMBL/DBD

A-Cross-references: EMBL:AC004095; NID:g2128465; PID:g212880

A-References: 1-496 -cDNA

R-Id: R. Paul, S.J. Lin, X. K. Kitchin, K.A. Croxby, M.L. Brandon, R.C. Sykes,

M. J. Fox, H. Mofat, K. J. Cronin, L. A. Sheu, M. J. Vanher, S. E. Talion, L.

Neu, 403/761-766, 1999

A-Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A-Accession: T00691 414480

A-Status: preliminary

A-Status: preliminary

A-Molecule type: DNA

A-Cross-references: EMBL:AC004095; NID:g2128465; PID:g212880

A-References: 1-496 -cDNA

R-Id: R. Paul, S.J. Lin, X. K. Kitchin, K.A. Croxby, M.L. Brandon, R.C. Sykes,

M. J. Fox, H. Mofat, K. J. Cronin, L. A. Sheu, M. J. Vanher, S. E. Talion, L.

Neu, 403/761-766, 1999

A-Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A-Accession: T00691 414480

A-Status: preliminary

A-Status: preliminary

A-Molecule type: DNA

Db 171 EYFQNDAPRDTQTSYVNM-GLSTGCMNVAVFPQPSRYVXVITL 225
 11
 Db 187 EYIN EDDMDQSPFRLDIEHSYVBNMNAHNFYQVCFPQDILSVKSYL 245
 Db 225 RAGSTNLSINSPDPTQYRKMDFQYVQVQVQVQVQVQVQVQVQV 264
 11
 Db 246 RRGVSTVLAADKPEFQVYKSLSDDFYVQVQVQVQVQVQVQVQVQV 305
 Db 285 SFPTVLAADKPEFQVYKSLSDDFYVQVQVQVQVQVQVQVQVQV 344
 11
 Db 306 TAPFVLAADKPEFQVYKSLSDDFYVQVQVQVQVQVQVQVQVQV 365
 Db 345 TLPDQVMAVQVYVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 404
 Db 366 VLDQVY.....QVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 433
 Db 405 GSNMKSIFDQVYVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 433
 Db 414 GSNMKSIFDQVYVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 442

RESULT 12

Hypothetical protein T1001.12 - Arabidopsis thaliana

T00691

C-Species: Arabidopsis thaliana (model-ear cross)

C-Date: 01-Feb-1999 Sequence-Revision 12-Feb-1999 tseq-Change 15-Jun-2001

R-Name: A12944110, S.D. Lau, S.J. Lin, X. K. Kitchin, K.A. Croxby, M.L. Brandon, R.C. Sykes,

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A-Cross-references: EMBL:AC004095; NID:g2128465; PID:g212880

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R-Id: R. Paul, S.J. Lin, X. K. Kitchin, K.A. Croxby, M.L. Brandon, R.C. Sykes,

M. J. Fox, H. Mofat, K. J. Cronin, L. A. Sheu, M. J. Vanher, S. E. Talion, L.

Neu, 403/761-766, 1999

A-Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A-Accession: T00691 414480

A-Status: preliminary

A-Status: preliminary

A-Molecule type: DNA

A-Cross-references: EMBL:AC004095; NID:g2128465; PID:g212880

A-References: 1-496 -cDNA

R-Id: R. Paul, S.J. Lin, X. K. Kitchin, K.A. Croxby, M.L. Brandon, R.C. Sykes,

M. J. Fox, H. Mofat, K. J. Cronin, L. A. Sheu, M. J. Vanher, S. E. Talion, L.

Neu, 403/761-766, 1999

A-Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A-Accession: T00691 414480

A-Status: preliminary

A-Status: preliminary

A-Molecule type: DNA

Db 171 EYFQNDAPRDTQTSYVNM-GLSTGCMNVAVFPQPSRYVXVITL 225
 11
 Db 187 EYIN EDDMDQSPFRLDIEHSYVBNMNAHNFYQVCFPQDILSVKSYL 245
 Db 225 RAGSTNLSINSPDPTQYRKMDFQYVQVQVQVQVQVQVQVQVQV 264
 11
 Db 246 RRGVSTVLAADKPEFQVYKSLSDDFYVQVQVQVQVQVQVQVQVQV 305
 Db 285 SFPTVLAADKPEFQVYKSLSDDFYVQVQVQVQVQVQVQVQVQV 344
 11
 Db 306 TAPFVLAADKPEFQVYKSLSDDFYVQVQVQVQVQVQVQVQVQV 365
 Db 345 TLPDQVMAVQVYVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 404
 Db 366 VLDQVY.....QVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 433
 Db 405 GSNMKSIFDQVYVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 433
 Db 414 GSNMKSIFDQVYVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 442

RESULT 13

Hypothetical protein T1001.12 - Arabidopsis thaliana

T00691

C-Species: Arabidopsis thaliana (model-ear cross)

C-Date: 01-Feb-1999 Sequence-Revision 12-Feb-1999 tseq-Change 15-Jun-2001

R-Name: A12944110, S.D. Lau, S.J. Lin, X. K. Kitchin, K.A. Croxby, M.L. Brandon, R.C. Sykes,

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A-References: 1-496 -cDNA

R-Id: R. Paul, S.J. Lin, X. K. Kitchin, K.A. Croxby, M.L. Brandon, R.C. Sykes,

M. J. Fox, H. Mofat, K. J. Cronin, L. A. Sheu, M. J. Vanher, S. E. Talion, L.

Neu, 403/761-766, 1999

A-Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A-Accession: T00691 414480

A-Status: preliminary

A-Status: preliminary

A-Molecule type: DNA

A-Cross-references: EMBL:AC004095; NID:g2128465; PID:g212880

A-References: 1-496 -cDNA

R-Id: R. Paul, S.J. Lin, X. K. Kitchin, K.A. Croxby, M.L. Brandon, R.C. Sykes,

M. J. Fox, H. Mofat, K. J. Cronin, L. A. Sheu, M. J. Vanher, S. E. Talion, L.

Neu, 403/761-766, 1999

A-Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A-Accession: T00691 414480

A-Status: preliminary

A-Status: preliminary

A-Molecule type: DNA

Genome version 5.1.3
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OM protein - protein search, using sw model

Run on: November 18, 2002, 14:37:47 / Search time 25 seconds

(without alignments) 885,934 Million cell updates/sec

Title: US-09-857-896a-32

Perfect score: 2784

Sequence: 1 M4C0EYFPAHATLPRFPMK.....VSSSLADLPFADSRFSQC 534

Scoring table: H2OSMK2

Gapop 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Library size 49 domains

Database: StalProc40.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	213.8	87	31	M4C0EYFPAHATLPRFPMK	US-09-857-896a-32
2	186.0	70.4	54.4	M4L1J0RNV	049973 hordeum vul
3	183.9	66.1	54.0	M4L1J0RNV	049973 hordeum vul
4	183.9	66.1	54.0	M4L1J0RNV	049973 hordeum vul
5	111.9	40.2	50.1	M4L1J0RNV	049973 hordeum vul
6	106.6	38.4	58.0	M4L1J0RNV	049973 hordeum vul
7	106.2	38.1	56.0	M4L1J0RNV	049973 hordeum vul
8	106.2	38.1	56.0	M4L1J0RNV	049973 hordeum vul
9	92.5	33.5	55.6	M4L1J0RNV	049973 hordeum vul
10	49.6	17.9	44.7	M4L1J0RNV	049973 hordeum vul
11	49.6	17.9	44.7	M4L1J0RNV	049973 hordeum vul
12	117.5	4.2	97.0	M4L1J0RNV	049973 hordeum vul
13	103.5	3.7	127.5	M4L1J0RNV	049973 hordeum vul
14	103.5	3.7	127.5	M4L1J0RNV	049973 hordeum vul
15	98.8	3.5	252.1	M4L1J0RNV	049973 hordeum vul
16	96.7	3.5	235.6	M4L1J0RNV	049973 hordeum vul
17	96.7	3.5	235.6	M4L1J0RNV	049973 hordeum vul
18	96.7	3.5	235.6	M4L1J0RNV	049973 hordeum vul
19	94.5	3.4	50.6	M4L1J0RNV	049973 hordeum vul
20	94.5	3.4	50.6	M4L1J0RNV	049973 hordeum vul
21	94.5	3.4	50.6	M4L1J0RNV	049973 hordeum vul
22	94.5	3.4	50.6	M4L1J0RNV	049973 hordeum vul
23	94.5	3.4	50.6	M4L1J0RNV	049973 hordeum vul
24	94.5	3.4	50.6	M4L1J0RNV	049973 hordeum vul
25	94.5	3.4	50.6	M4L1J0RNV	049973 hordeum vul
26	94.5	3.4	50.6	M4L1J0RNV	049973 hordeum vul
27	94.5	3.4	50.6	M4L1J0RNV	049973 hordeum vul
28	94.5	3.4	50.6	M4L1J0RNV	049973 hordeum vul
29	94.5	3.4	50.6	M4L1J0RNV	049973 hordeum vul
30	94.5	3.4	50.6	M4L1J0RNV	049973 hordeum vul
31	94.5	3.4	50.6	M4L1J0RNV	049973 hordeum vul
32	94.5	3.4	50.6	M4L1J0RNV	049973 hordeum vul
33	94.5	3.4	50.6	M4L1J0RNV	049973 hordeum vul

34	87.5	3.1	100.0	1	DEPL10RNV	P23357 equine hsp
35	87.5	3.1	126.6	1	YCP11RNV	P57368 human hsp
36	87.5	3.1	126.6	1	YCP11RNV	P57368 human hsp
37	87.5	3.1	126.6	1	YCP11RNV	P57368 human hsp
38	87.5	3.1	126.6	1	YCP11RNV	P57368 human hsp
39	87.5	3.1	126.6	1	YCP11RNV	P57368 human hsp
40	87.5	3.1	126.6	1	YCP11RNV	P57368 human hsp
41	87.5	3.1	126.6	1	YCP11RNV	P57368 human hsp
42	87.5	3.1	126.6	1	YCP11RNV	P57368 human hsp
43	87.5	3.1	126.6	1	YCP11RNV	P57368 human hsp
44	87.5	3.1	126.6	1	YCP11RNV	P57368 human hsp
45	87.5	3.1	126.6	1	YCP11RNV	P57368 human hsp

ALIGNMENTS

1	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
2	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
3	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
4	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
5	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
6	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
7	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
8	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
9	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
10	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
11	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
12	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
13	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
14	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
15	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
16	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
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18	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
19	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
20	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
21	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
22	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
23	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
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27	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
28	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
29	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
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31	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
32	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
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36	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
37	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
38	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
39	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
40	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
41	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
42	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
43	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
44	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA
45	M4C0EYFPAHATLPRFPMK	STANDARD	PRF	533 AA

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misleading, and that the European Bioinformatics Institute is acknowledged

or send an email to license@ebi.ac.uk.

EMBL, Y14573; CNA74909.1; .

InterPro: IPR004370; M0.

Protein domain: Transmembrane; Pathogenesis-related protein.

Transmembrane: 18

POTENTIAL: 38

POTENTIAL: 132

50 SEQUENCE 576 AA; 6548 MW; 430AF6AD640856 CHECK;
 QUERY MATCH 46.0%; Score 1281.5; DB 1; Length 576;
 11 RFLPETSFMALVAVNYVITLLEALIMKGLNHRNNAALATKELMILW 70
 6 RLESLPFAVAVNYVITLLEALIMKGLNHRNNAALATKELMILW 65
 71 ISLLATPDPISGICISERKAKIMRCPSPGVSKYK-KDY- 113
 66 ISLLATPDPISGICISERKAKIMRCPSPGVSKYK-KDY- 113
 114 -----CANGKVMSTGSCIMDITFEYLAHNYVITLLEALIMKGLN 160
 124 SPRNMAKATGICDCKAKVLAALAGIDITFEYLAHNYVITLLEALIMKGLN 183
 161 KMTETFALEVNADPAPRFTNQTSPVRIHL-STRGIMVAVPQSPGVSKYK 243
 184 KMTETFALEVNADPAPRFTNQTSPVRIHL-STRGIMVAVPQSPGVSKYK 243
 220 DITLAKGTINMANS-KEFYRYSKMDQRYVAVVGLKMLVLELID 277
 244 DITLAKGTINMANS-KEFYRYSKMDQRYVAVVGLKMLVLELID 277
 278 TGLVNTSLVITLLEALIMKGLNHRNNAALATKELMILW 337
 304 MWSLMLPELITLLEALIMKGLNHRNNAALATKELMILW 363
 338 VFTFTIDPQVNAHNYVITLLEALIMKGLNHRNNAALATKELMILW 397
 364 IFTLHVLFTNAHNYVITLLEALIMKGLNHRNNAALATKELMILW 427
 398 VALVQWSTNKRFTIDPQVNAHNYVITLLEALIMKGLNHRNNAALATKELMILW 457
 424 VALVQWSTNKRFTIDPQVNAHNYVITLLEALIMKGLNHRNNAALATKELMILW 457
 458 PARSAPVILKAKOMRQDQ-----SAPSPRMEKMDQRYVAVVGLKMLVLELID 513
 476 PARSAPVILKAKOMRQDQ-----SAPSPRMEKMDQRYVAVVGLKMLVLELID 513
 514 SVSSALMDQ-----PARAPS 530
 531 STQREIDSEFNSHIDQMA 552

50 SEQUENCE 501 AA; 56896 MW; 487950F718C78 CHECK;
 QUERY MATCH 40.2%; Score 1119; DB 1; Length 501;
 11 RFLPETSFMALVAVNYVITLLEALIMKGLNHRNNAALATKELMILW 70
 15 RLESLPFAVAVNYVITLLEALIMKGLNHRNNAALATKELMILW 65
 71 ISLLATPDPISGICISERKAKIMRCPSPGVSKYK-KDY- 113
 66 ISLLATPDPISGICISERKAKIMRCPSPGVSKYK-KDY- 113
 114 -----CANGKVMSTGSCIMDITFEYLAHNYVITLLEALIMKGLN 160
 124 SPRNMAKATGICDCKAKVLAALAGIDITFEYLAHNYVITLLEALIMKGLN 183
 161 KMTETFALEVNADPAPRFTNQTSPVRIHL-STRGIMVAVPQSPGVSKYK 243
 184 KMTETFALEVNADPAPRFTNQTSPVRIHL-STRGIMVAVPQSPGVSKYK 243
 220 DITLAKGTINMANS-KEFYRYSKMDQRYVAVVGLKMLVLELID 277
 244 DITLAKGTINMANS-KEFYRYSKMDQRYVAVVGLKMLVLELID 277
 278 TGLVNTSLVITLLEALIMKGLNHRNNAALATKELMILW 337
 304 MWSLMLPELITLLEALIMKGLNHRNNAALATKELMILW 363
 338 VFTFTIDPQVNAHNYVITLLEALIMKGLNHRNNAALATKELMILW 397
 364 IFTLHVLFTNAHNYVITLLEALIMKGLNHRNNAALATKELMILW 427
 398 VALVQWSTNKRFTIDPQVNAHNYVITLLEALIMKGLNHRNNAALATKELMILW 457
 424 VALVQWSTNKRFTIDPQVNAHNYVITLLEALIMKGLNHRNNAALATKELMILW 457
 458 PARSAPVILKAKOMRQDQ-----SAPSPRMEKMDQRYVAVVGLKMLVLELID 513
 476 PARSAPVILKAKOMRQDQ-----SAPSPRMEKMDQRYVAVVGLKMLVLELID 513
 514 SVSSALMDQ-----PARAPS 530
 531 STQREIDSEFNSHIDQMA 552

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01	168	AMERIN	-----RFTFTTSSPEPHALILSTETGSRMAVPSFQPSFSTVY--	d 320
02	169	CLADO	-----PFTNFTTSLKALVYVLTSLDQV--	d 320
03	221	CLADO	-----QALMLAIVSTFTFFSVISVLTSLVSSSSQAMVLTQVQALATSSN	695
04	221	CLADO	-----RT--NN--LNNPFT--	811
05	221	CLADO	-----RT--NN--LNNPFT--	811
06	246	REMNODOR	-----KVVVGLAKMLKAVLTLELDGQIGVNTSFFPFLKACVQKMLTME	105
07	246	REMNODOR	-----KVVVGLAKMLKAVLTLELDGQIGVNTSFFPFLKACVQKMLTME	105
08	656	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
09	736	MAEVSQSSN	-----VSLVLAALCLGVRGSLVSTSLVSTSLVSTSLVSTSLVSTSLV	176
10	736	MAEVSQSSN	-----VSLVLAALCLGVRGSLVSTSLVSTSLVSTSLVSTSLVSTSLV	176
11	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
12	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
13	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
14	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
15	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
16	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
17	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
18	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
19	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
20	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
21	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
22	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
23	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
24	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
25	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
26	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
27	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
28	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
29	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
30	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
31	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
32	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
33	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
34	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
35	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
36	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
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41	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
42	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
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44	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
45	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
46	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
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51	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
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54	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
55	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
56	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
57	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
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59	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157
60	812	VSLSTSTSD	-----LVPTVYKHOHPLKNNKLTFLKAVLLAQVAVLYVDPRLTET	157

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